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TITLE: Genomic and Expression Profiling of Benign and Malignant Nerve Sheath Tumors in Neurofibromatosis Patients

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14. ABSTRACT The goal of the study is to identify genes that will serve as molecular markers for progression of neurofibroma to MPNST, and to identify potential therapeutic targets. miRNA expression profiling was performed on 6 cases of MPNSTs, and 7 cases of synovial sarcomas. By using unsupervised hierarchical clustering most tumors were grouped together according to tumor type. Subsequent analyses using Significance Analysis of Microarrays (SAM) identified miRNAs that differentiate between MPNSTs and synovial sarcoma (SS). To develop a cell line model for MPNSTs, global gene expression profiles for cell lines established from 3 primary MPNST and SS tumor tissues was carried out and their expression profiles were compared with other sarcomas. A large tissue microarray (TMA) containing about 200 nerve sheath tumors was used to test for EGFR expression by IHC. Neoplasms in which the majority of samples showed high expression by IHC included MPNST (83% of NF1-associated and 77% of sporadic), 73% of plexiform neurofibroma, 100% diffuse neurofibroma and 93% of SS.					
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**Title: Genomic and Expression Profiling of Benign and Malignant Nerve Sheath Tumors in Neurofibromatosis Patients.**

## **INTRODUCTION**

Neurofibromatosis Type 1 (NF1) affects 1:3000 live births and can be inherited as an autosomal dominant trait that is caused by mutations in the NF1 gene or acquired by a de novo mutation in this gene. There is a significant risk of developing malignancies, the vast majority of which are malignant peripheral nerve sheath tumors (MPNST). The incidence of malignant transformation in patients with NF1 is ~5%. These tumors are aggressive sarcomas and are associated with a 5-year survival rate of ~40%. Malignant transformation is not easy to identify but can be associated with the occurrence of pain and growth in a preexisting neurofibroma. The number of neurofibromas that patients typically have and their location make screening for transformation to MPNST difficult and therefore the MPNSTs are often found at a late clinical stage (Weiss and Goldblum, 2001).

Our extensive messenger RNA expression profile data show unexplained down regulation of gene expression as being one of the most prominent features of the transition of NF to MPNST (see 3<sup>rd</sup> annual report). We hypothesize that microRNA (miRNA) expression differences, as yet unstudied in NF and MPNST, may play a central role in these findings. Recent studies suggest that knowledge of miRNA expression patterns in cancer may have substantial value for diagnostic and prognostic determinations as well as for eventual therapeutic intervention (Calin and Croce, 2006; Calin *et al.*, 2005; Esquela-Kerscher and Slack, 2006). MicroRNAs (miRNAs) are a class of conserved, noncoding RNAs, composed of single-stranded RNAs of ~ 19-22 nucleotides. These regulatory small RNAs play a role in gene regulation (Lau *et al.*, 2001) through RNA interference (RNAi) mechanisms. Functionally, miRNAs can inhibit the protein synthesis from a wide variety of mRNAs through either inhibition of translation by imperfect base-pairing with their target mRNA at the 3'UTR or by inducing cleavage of target mRNA through perfect complementary sequence base-pairing (Bartel, 2004; Doench and Sharp, 2004).

In the last year we have extensively worked on standardization of microRNA expression profiling using the microRNA microarrays printed at the Stanford functional genome facility. We have profiled the miRNA expression for 6 MPNSTs and 7 synovial sarcomas (a tumor in the differential diagnosis). In collaboration with the laboratory of Dr. Andy Fire, who recently was awarded the Nobel Prize for his work on miRNA, we also cloned and sequenced the small

RNA from a MPNST and a neurofibroma case; we also cloned miRNAs from 2 cases of synovial sarcomas.

## **BODY**

### **Specific aim 1: Genome wide search for genes in nerve sheath tumor**

#### **A1. Standardization of miRNA expression profiling**

miRNA microarrays used in the study were printed at the Stanford Functional Genomics Facility. The arrays contained a total of 668 probes spotted in duplicate. The 668 probes represent 328 known human miRNAs, 113 mouse miRNAs, 45 rat miRNAs, 154 predicted human miRNAs and 28 control probes (Ambion, Austin, Texas). Since the regular (TRIzol) method eliminates the small RNA species, the miRNA isolation procedure from frozen tissue samples had to be modified. Our objective was to isolate the total RNAs that included the small RNA species so that the RNA obtained by this procedure will be used in both messenger RNA arrays and for miRNA arrays. In our final protocol, total RNA is extracted from frozen tumor samples using the mirVana™ miRNA isolation kit (Ambion, Austin, Texas) with modifications to isolate up to 250 ug of total RNA. Further, using a proper 'Reference RNA' for the array expression is an important step in developing a protocol for miRNA arrays. After testing reference RNA samples from many vendors, we identified reference RNA (XpressRef™ Universal Total RNA) obtained from SuperArray (Frederick, MD) as having a high quality and quantity of small RNA species. miRNA was further enriched from 25 µg of total RNA using a microcon YM-100 column (Millipore, Billerica, MA), and indirectly labeled with Cy3 or Cy5 amine reactive dyes (Amersham, Buckinghamshire, UK) using mirVana™ miRNA labeling kit (Ambion). Post-processing of arrays and washing conditions were modified to obtain high quality of data. Hybridization was at 42°C for 12-16 hrs. Arrays were washed and immediately scanned using a GenePix 4000B array scanner (Axon Instruments, Foster City, CA).

#### **A2. miRNA expression profiling and analysis**

The miRNA expression profile for 6 MPNST cases was determined and compared to 7 synovial sarcomas (SS). Fluorescence ratios (sample/reference) were calculated using GenePix software and miRNA arrays were normalized. To limit the measurement errors, only miRNA spots with a ratio of signal over background of at least 2 in both Cy3 and Cy5 channels were included. Further, miRNA spots were filtered based on those where expression levels differed by at least four-fold in at least two arrays. Finally miRNA spots with 80% good data were selected. As a first step in the analysis, we asked whether the miRNA expression signatures of these tumor types were distinct. The 60 miRNAs that met the filtering criteria were subjected to hierarchical clustering among these 13 sarcomas in an unsupervised manner. The clustering algorithm grouped both miRNAs and samples into clusters based on overall similarity in miRNA

expression pattern without prior knowledge of sample identity. Clustering based on the 60 miRNAs revealed substantive distinctions in overrepresented and underrepresented miRNAs among the tumors (Figure 1). As is evident from the dendrogram at the top of the heat map, the tumors clustered into 2 main groups, whereby all MPNSTs and SS separated into two distinct groups.

### **A3. Significance Analysis of Microarrays**

Using SAM analysis, we identified the miRNAs that distinguished MPNST from synovial sarcomas. A total of 14 miRNAs showed significant relative overrepresentation in MPNSTs compared to SS. Five miRNAs showed relative underrepresentation in MPNSTs. The results for the top miRNAs of each class with <2% FDR (false discovery rate) are detailed in Table 1.

### **A4. Small RNA isolation, cloning and analysis**

Small RNA extracted using mirVana<sup>TM</sup> miRNA isolation kit (Ambion) was used as starting material for cloning procedure of Lau *et al* (Lau *et al.*, 2001) with slight modifications. Purified small RNAs were ligated with pre-adenylylated 3'-adaptor oligonucleotide, gel purified, and subjected to a second ligase reaction with a 5'-adaptor oligonucleotide. The gel-purified, doubly-ligated RNA was reversed transcribed using Superscript II (Invitrogen, Carlsbad, CA) and RT primer, followed by PCR amplification using the RT primer and a forward primer. A second PCR was performed using the RT primer and a second forward primer. The PCR product was purified by phenol/chloroform extractions and then digested with Ban I (NEB, Beverly, MA) for concatemerization using T4 DNA ligase (NEB). Concatamers ranging from 600-1000 bp were isolated from a low-melting-point agarose gel, processed with Taq polymerase, and cloned into the pCR4-TOPO vector using the TOPO TA cloning kit (Invitrogen). Colony PCR was performed using the M13 forward and reverse primers, and the PCR products were prepared for sequencing using shrimp alkaline phosphatase and exonuclease I (USB Corporation, Cleveland, Ohio). Small RNAs obtained by cloning were compared with functionally annotated sequences using BLAST (blastn, <http://www.ncbi.nlm.nih.gov/blast/>), BLAT (<http://genome.ucsc.edu>), miRBase and simple text searches. For each cloned small RNA, the best alignments to a functionally annotated sequence (not more than one error) were used to assign a functional category to the small RNA. Putative novel small RNAs were analyzed using mfold version 3.2 (Zuker, 2003) to identify potential precursor structures.

miRNA were cloned and sequenced from small RNA libraries of 4 sarcomas (1 MPNST, 1 NF and 2 SS) tissues. A total of 1681 small RNA clones were sequenced, of which 94 could be annotated as known miRNAs (Tables 2 and 3).

#### **A5. Gene expression profiles of MPNST and synovial sarcoma cell lines established from primary tumors.**

Cell lines derived from fresh tumors have been widely used as experimental models to understand the biology of tumor progression and other treatment strategies. Dr Jonathan Fletcher at Brigham and Women's Hospital, Harvard Medical School has established 31 sarcoma cell lines that included 3 MPNSTs and 3 synovial sarcomas. In collaboration with his group we have characterized the global gene expression profiles for 3 MPNST and 3 synovial sarcoma cell lines using HEEBO arrays and compared the expression profiles of these tumors with the other sarcoma cell lines. Unsupervised hierarchical analysis clustered the gene array data from 31 cell lines broadly clustered the cell lines based on the tumor-type (Figure 2). Two of the three MPNST cell lines clustered together and all the 3 synovial sarcoma cell line formed a tight cluster. The preliminary data on the gene expression profiles of these cell lines was presented as a poster in the 2007 annual meeting of United States and Canadian Academy of Pathology (USCAP; see appendix 1). We are currently in the process of comparing the data generated from primary MPNST and SS tumors to the MPNST and SS cell lines.

#### **Specific Aim 2: Validation of candidate genes on large numbers of cases using immunohistochemistry and *in situ* hybridization on TMA.**

TMA's form excellent tools to validate and extend findings from gene array studies since paraffin-embedded archival material is much easier to collect than fresh frozen material. The TMA was constructed as part of a close collaboration between the Stanford group and the funded collaborators at University of Washington (Brian Rubin) and University of British Columbia (Torsten Nielsen) (see annual reports 2 and 3). As a result we now have access to what to our knowledge is the largest TMA of nerve sheath tumors. This TMA (TA-138) contains 68 MPNSTs, 42 neurofibromas, 22 schwannomas and 15 synovial sarcomas. All the cases were represented in duplicate cores of 0.6mm diameter.

#### **Attempts to develop ISH probes for miRNA**

We have had good success confirming gene expression profiling studies using non-radioactive miRNA probes for in situ hybridization (ISH) in formalin-fixed paraffin-embedded (FFPE) tissue. While the cloning experiments described above form an independent validation of the array-based miRNA studies further confirmation is obtainable if we could use ISH for miRNA or FFPE. This would also have the benefit of allowing us to precisely identify the cell type for which the miRNA signal from which this miRNA signal originates that we see in lysates of whole tumors. In the past year we have spent considerable effort in optimizing our ISH protocol for mRNA to one that could detect mirRNA.

Since miRNA species are extremely short (19-22 nucleotides) we decided to generate LNA probes for these molecules. LNA has a much higher melting temperature than RNA and thus seems optimal for these studies.

We have been able to obtain very strong signals using these probes but are still struggling with background problems. Most of our experience is based on work with LNA probes miR143 and miR21. In our next set of experiments we will extend this number of probes and the variables under which they are tested.

### **EGFR expression studies using nerve sheath tumor tissue array.**

Epidermal growth factor receptor (EGFR), located at 7p12, is a member of a protein tyrosine kinase family and functions as a cell cycle regulatory protein. The receptor is activated by the binding of epidermal growth factor (EGF) and transforming growth factor, which leads to receptor autophosphorylation resulting in cell proliferation and cell survival through inhibition of apoptosis and promotion of angiogenesis. The multiple cellular signaling interactions of EGFR biology allows for potential EGFR inhibitors to counteract cellular proliferation, angiogenesis, invasion and metastasis. From the gene array data we have identified EGFR that was highly expressed in a significant subset of MPNSTs. Using TA-138 we have studied the differential expression of EGFR in a larger number of cases of PNSTs (see the attached manuscript). Figure 3A-D shows examples of EGFR staining in PNSTs showing 3+ reactivity to EGFR, with >50% of the tumor cells having intense membrane staining. Figure 4 shows an example of EGFR amplification in MPNST. The detailed analyses of EGFR expression in PNSTs are given in appendix 2.

## **KEY RESEARCH ACCOMPLISHMENTS**

1. Standardization of miRNA expression profiling using miRNA microarrays
  - Bioinformatical and statistical analyses.
  - Identification of miRNAs that distinguish MPNSTs from synovial sarcomas
2. EGFR expression profiling in PNSTs.
3. Global gene expression profiling of novel MPNST and SS cell lines established from primary tumors

## **REPORTABLE OUTCOMES:**

Publication



AJ Larson, E Downs-Kelly, M Skacel, RR Tubbs, BP Rubin, M van de Rijn, RB West, C Corless, A Chiesa and JR Goldblum. Epidermal growth factor receptor (EGFR) expression and gene amplification spectrum of spindle cell soft tissue neoplasms. A fluorescence in situ hybridization (FISH) and immunohistochemical study (in press 2007).

Abstract

Poster presentation at the 2007 annual meeting of USCAP.

## **CONCLUSIONS**

In the past year we standardized and performed miRNA microarray analysis on 6 MPNSTs and 7 synovial sarcomas. We believe that the study of miRNA expression in these tumors may lead to a better understanding of the differences in gene expression profiles we observed using our mRNA expression profiling studies.

We have carried out extensive bioinformatic analysis to annotate the miRNAs and we are preparing to study a larger number of tumors.

We believe that in addition to explaining the biology of NF-MPNST transformation miRNAs can be exploited to be used in the diagnosis of MPNSTs

Standardizing methods to use LNA based ISH on FFPE tissues.

TMA's were used to study the expression of EGFR in PNSTs and showed that the disparity between EGFR protein overexpression and the paucity of EGFR gene amplification may be secondary to some post-transcriptional modification. The finding of EGFR overexpression, especially in malignant neoplasms, deserves further study as EGFR antagonists may be of benefit to patients with soft tissue tumors that express and are dependent on EGFR.

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## LEGENDS FOR FIGURES

### Figure 1

Unsupervised hierarchical clustering analysis of 6 MPNSTs and 7 SS cases based on miRNA expression. Each row represents the relative levels of expression for a single miRNA and each column shows the expression levels for a single sample. The red or green color indicates relatively high or low expression, respectively, while grey indicates absent datapoints. The two main groups of the dendrogram labeled as A (MPNST) and B (SS) separated the tumors.

### Figure 2

Unsupervised hierarchical clustering analysis for mRNA gene expression profiling of 3 MPNSTs and 3 SS cell line established from the fresh tumors. The MPNSTs are color coded with blue and SS with red. The expression profiles of MPNSTs and SS are compared with 25 other sarcoma samples.

### Figure 3A-E, Immunohistochemistry staining for EGFR.

- A) MPNST showing 3+ reactivity to EGFR, with >50% of the tumor cells having intense membrane staining.
- B) Example of 2+ immunoreactivity in a plexiform NF with moderate staining in >10% of tumor cells.
- C) Example of 1+ immunoreactivity in a NF with weak staining in <10% of tumor cells (magnification 200x, inset 400x).
- D) Example of a synovial sarcoma with 3+ reactivity to EGFR, with >50% of the tumor cells showing diffuse membrane staining.
- E) Example of a Schwannoma with no immunoreactivity to EGFR (magnification 200x )

Figure 4. Example of a MPNST with EGFR amplification. The centromeric probe (CEP7), directed against 7p11.1-q11.1, emits two green fluorescent signals per nucleus, while the EGFR probe, directed against 7p12 fluoresces orange and shows multiple copies of the EGFR gene. In this case, the EGFR/CEP7 ratio was 4.2. Example of a MPNST with polysomy 7, in this example the chromosome copy number average was 5.5.

## APPENDICES

**Appendix 1: Abstract**

Gene expression profiling of 24 Novel sarcoma cell lines

CH Lee, S Zhu, M van de Rijn, JA Fletcher. Stanford University, Stanford, CA;  
Brigham and Women's Hospital, Boston, MA Annual meeting USCAP 2007.

**Appendix 2: Manuscript**

Epidermal growth factor receptor (EGFR) expression and gene amplification  
spectrum of spindle cell soft tissue neoplasms. A fluorescence in situ  
hybridization (FISH) and immunohistochemical study (in press 2007).

Figure 1

Figure 1 displays hierarchical clustering of miRNAs. The top dendrogram (A and B) shows clustering of miRNAs into two main groups, A (blue) and B (red). The bottom dendrogram shows clustering of miRNAs into two main groups, A (blue) and B (red). The heatmap shows the expression levels of miRNAs across two conditions, A and B. The color scale ranges from green (low expression) to red (high expression). The miRNAs are listed on the right side of the heatmap.

MicroRNAs (miRNAs) listed on the right side of the heatmap (from top to bottom):

- HSA-MIR-200C
- HSA-MIR-203
- MMU-MIR-203
- HSA-ABI-2637
- MMU-MIR-222
- HSA-MIR-197
- HSA-MIR-520G
- HSA-MIR-512-3P
- HSA-MIR-517A
- HSA-MIR-517B
- HSA-MIR-100
- HSA-MIR-99A
- MMU-MIR-99A
- HSA-ABI-1326B
- HSA-MIR-92
- HSA-MIR-220
- HSA-MIR-9\*
- HSA-MIR-342
- HSA-MIR-126
- HSA-LET-7B
- HSA-LET-7C
- HSA-LET-7D
- HSA-LET-7A
- MMU-LET-7A
- HSA-LET-7E
- HSA-LET-7F
- MMU-LET-7F
- HSA-MIR-26A
- HSA-MIR-16
- HSA-ABI-1310B
- MMU-MIR-140\*
- HSA-MIR-21
- HSA-MIR-29A
- HSA-MIR-29B
- HSA-MIR-23A
- HSA-MIR-23B
- HSA-MIR-27B
- HSA-MIR-24
- MMU-MIR-10B
- HSA-MIR-10B
- HSA-MIR-199A\*
- HSA-MIR-10A
- HSA-MIR-497
- HSA-MIR-195
- HSA-MIR-315
- HSA-MIR-223
- HSA-MIR-451
- MMU-MIR-451
- HSA-MIR-133A
- HSA-MIR-133B
- HSA-MIR-206
- RNO-MIR-1
- HSA-MIR-146B
- HSA-MIR-155
- HSA-MIR-199B
- HSA-MIR-9
- MMU-MIR-106A
- HSA-MIR-20B

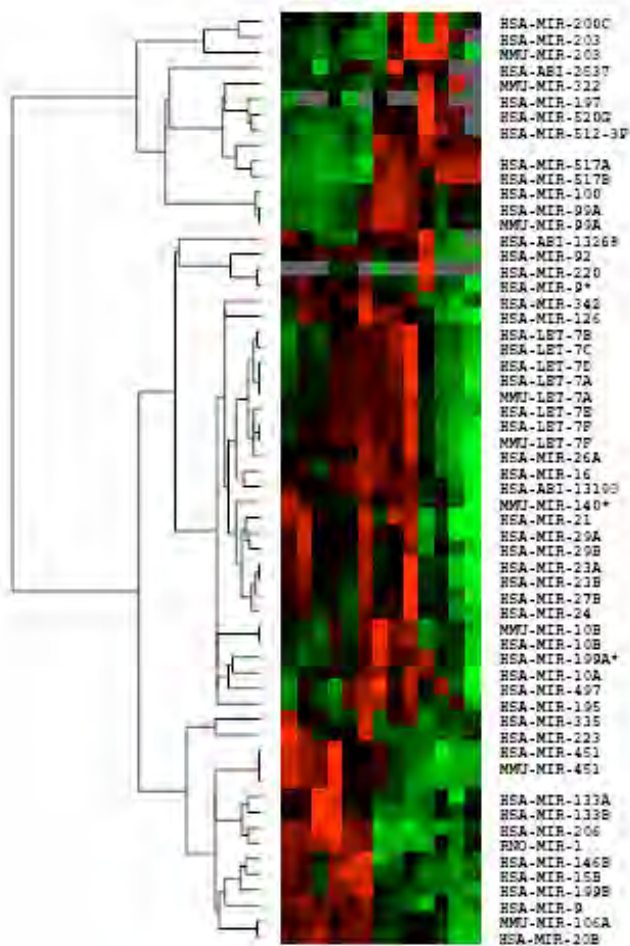


Figure 2

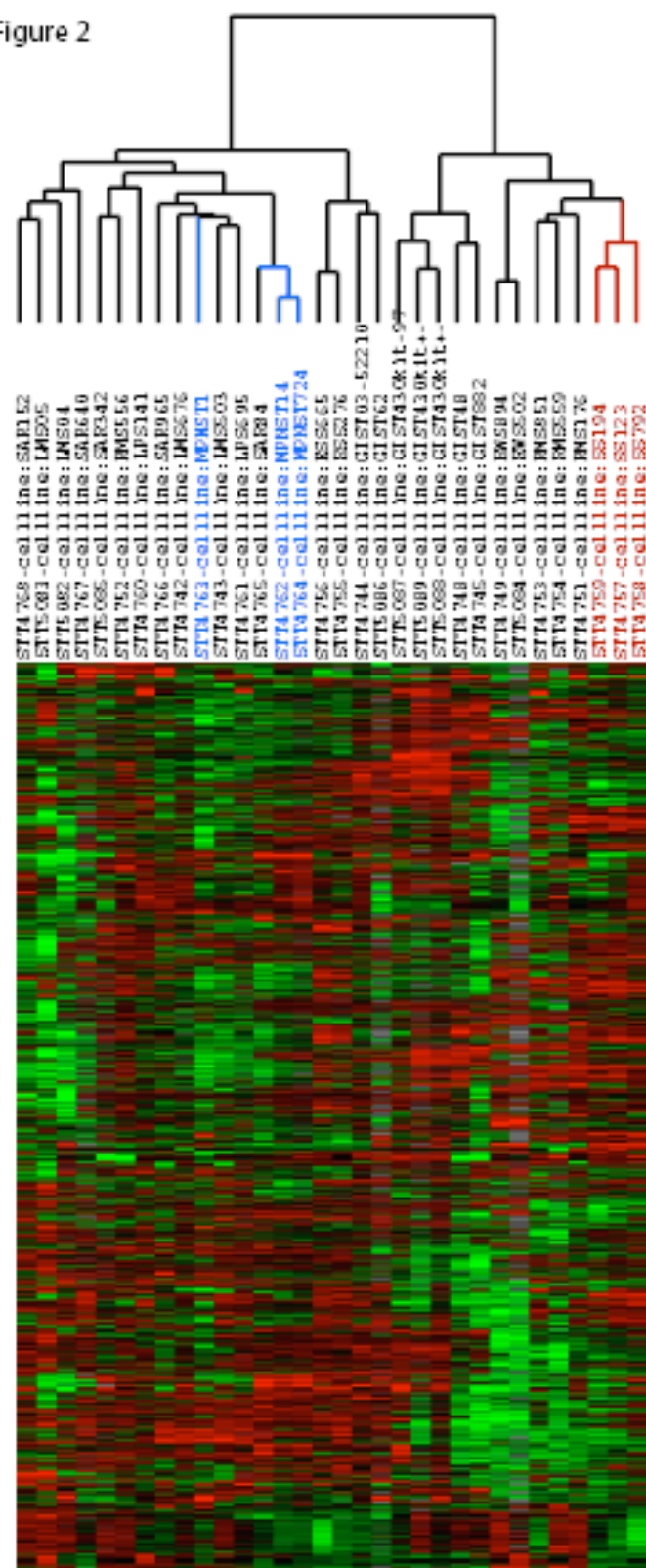


Figure 3A-C

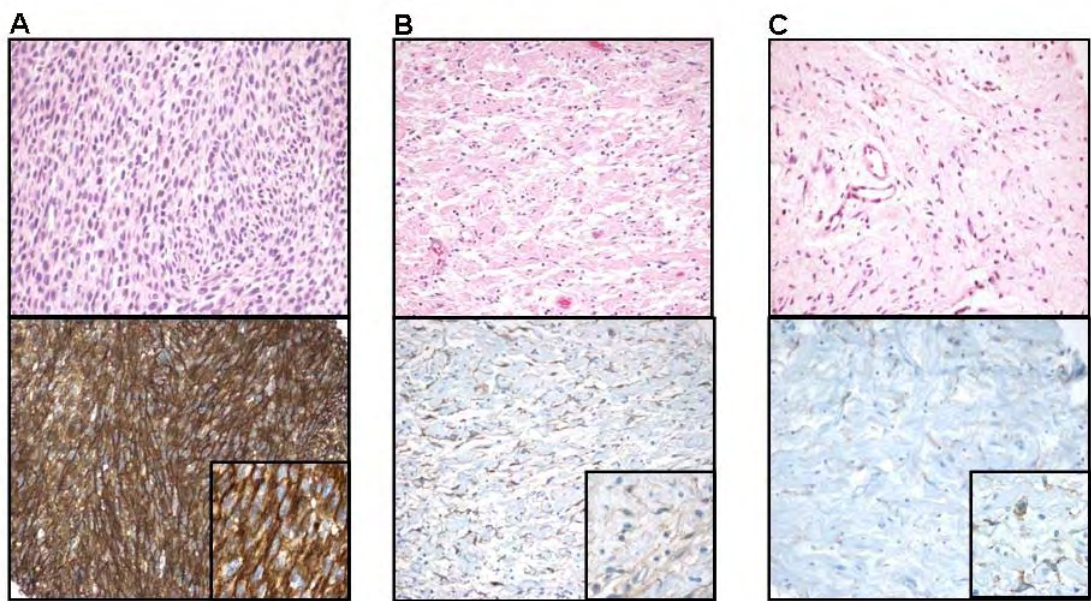


Figure 3D-E

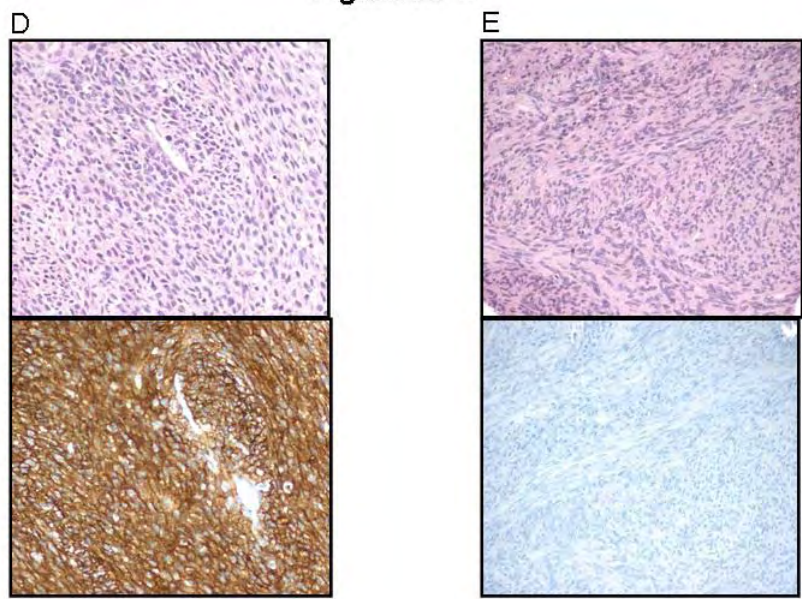
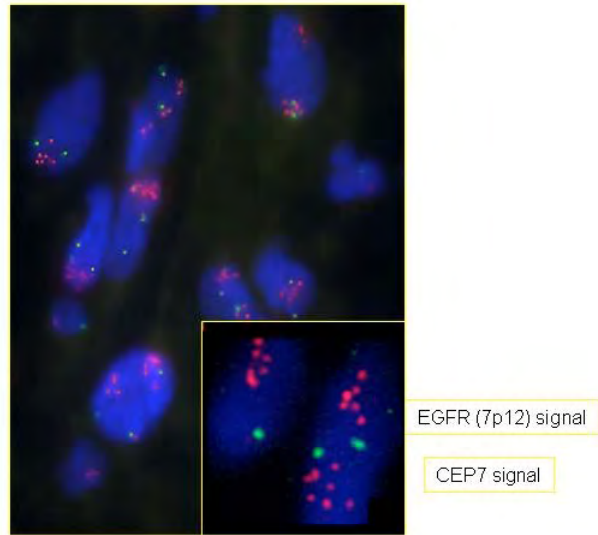


Figure 4





**Table 1: Significance analysis of miRNA expression of MPNST**

Gene ID	Score(d)	Fold Change	q-value(%)
HSA-MIR-206	4.394659	29.62	0
HSA-MIR-9	3.288742	5.18	0
HSA-MIR-146B	3.000959	8.57	0
HSA-MIR-15B	2.890168	7.84	0
HSA-MIR-451	2.630717	7.94	0
HSA-MIR-20B	2.62999	4.17	0
HSA-MIR-199B	2.397392	5.70	0
HSA-MIR-223	2.355982	7.89	0
HSA-MIR-133A	2.350066	9.28	0
HSA-MIR-133B	2.310541	8.00	0
HSA-MIR-21	1.495222	2.10	0
HSA-MIR-342	1.417306	2.38	1.94
HSA-MIR-29A	1.351994	1.96	1.94
HSA-MIR-29B	1.349319	2.31	1.94
HSA-MIR-517A	-5.51924	0.09	0
HSA-MIR-517B	-4.93106	0.06	0
HSA-MIR-512-3P	-2.58844	0.12	0
HSA-MIR-520G	-2.31417	0.17	0
HSA-MIR-100	-1.99153	0.25	0

**Table2. Small RNA composition of the cDNA libraries prepared from 4 human soft tissue tumors**

Type	SS1		SS2		NF		MPNST	
	no.	%	no.	%	no.	%	no.	%
previously identified miRNAs	741	90.6	637	78.0	99	56.6	206	87.3
Class I (candidate miRNA)	2	0.2	3	0.4	0	0	0	0
Class II (candidate small RNA with non-canonical hairpin)	0	0	0	0	0	0	0	0
Class III (candidate small RNA without significant hairpin)	0	0	0	0	2	1.1	1	0.4
rRNA	17	2.1	35	4.3	44	25.1	14	5.9
tRNA	18	2.2	131	16.0	13	7.4	8	3.4
sn/sno/misc-RNA	9	1.1	5	0.6	4	2.3	1	0.4
mitochondrial	24	2.9	1	0.1	0	0	0	0
repeat	2	0.2	0	0	3	1.7	0	0
mRNA	0	0.0	0	0	0	0	2	0.8
not mapped/ unknown	5	0.6	5	0.6	10	5.7	4	1.7
total number of sequences	818	100	817	100	175	100	236	100

**Table 3: Annotated miRNAs of MPNSTs and SS samples**

miRNA	638 (SS)		1739 (SS)		4536 (NF)		3922 (MPNST)	
	no.	%	no.	%	no.	%	no.	%
let-7a	55	7.4	4	0.6	14	14.1	12	5.8
let-7b	295	39.8	118	18.5	27	27.3	62	30.1
let-7c	32	4.3	37	5.8	1	1.0	15	7.3
let-7d		0.0		0.0	1	1.0	4	1.9
let-7d*		0.0	1	0.2		0.0		0.0
let-7e	8	1.1		0.0		0.0	1	0.5
let-7f	16	2.2	6	0.9	6	6.1	12	5.8
let-7f*		0.0	1	0.2		0.0		0.0
let-7g	5	0.7		0.0	1	1.0	2	1.0
let-7i	6	0.8	30	4.7	2	2.0	8	3.9
miR-15a	1	0.1	1	0.2		0.0		0.0
miR-16	3	0.4		0.0		0.0		0.0
miR-19b		0.0	2	0.3		0.0		0.0
miR-21	41	5.5	16	2.5	20	20.2	43	20.9
miR-22		0.0	2	0.3		0.0		0.0
miR-23a	12	1.6		0.0		0.0		0.0
miR-23b	11	1.5	2	0.3		0.0	3	1.5
miR-24	5	0.7	4	0.6		0.0		0.0
miR-25	1	0.1		0.0		0.0		0.0
miR-26a	11	1.5	1	0.2	1	1.0		0.0
miR-26b	5	0.7		0.0		0.0		0.0
miR-27a	14	1.9	2	0.3		0.0	3	1.5
miR-27b	16	2.2	1	0.2		0.0	2	1.0
miR-29a	1	0.1	1	0.2		0.0		0.0
miR-34a	1	0.1		0.0		0.0		0.0
miR-92	6	0.8		0.0	1	1.0	1	0.5
miR-92b		0.0		0.0		0.0	1	0.5
miR-93		0.0	3	0.5		0.0		0.0
miR-99a	2	0.3	5	0.8		0.0		0.0
miR-99b	7	0.9	1	0.2		0.0	1	0.5
miR-100	6	0.8	5	0.8		0.0	1	0.5
miR-103		0.0	1	0.2		0.0		0.0
miR-106b	1	0.1		0.0		0.0		0.0
miR-124a		0.0	12	1.9		0.0		0.0
miR-125a	7	0.9		0.0	2	2.0	1	0.5
miR-125b	49	6.6	16	2.5	10	10.1	11	5.3
miR-126		0.0	2	0.3		0.0		0.0
miR-126*	2	0.3		0.0		0.0		0.0
miR-127	9	1.2	41	6.4		0.0		0.0
miR-128b		0.0		0.0	1	1.0		0.0
miR-130a	4	0.5	2	0.3		0.0	1	0.5
miR-135a		0.0	1	0.2		0.0		0.0
miR-136		0.0	1	0.2		0.0		0.0
miR-140		0.0	2	0.3		0.0		0.0
miR-143	1	0.1	1	0.2		0.0		0.0
miR-146a		0.0		0.0	2	2.0		0.0
miR-148b		0.0	1	0.2		0.0		0.0
miR-151		0.0	4	0.6		0.0	1	0.5
miR-151*	25	3.4	38	6.0	7	7.1	5	2.4
miR-154	9	1.2	3	0.5		0.0		0.0
miR-181a	1	0.1	5	0.8		0.0		0.0
miR-181b		0.0	1	0.2		0.0		0.0
miR-182		0.0	2	0.3		0.0		0.0
miR-183		0.0	1	0.2		0.0		0.0
miR-185		0.0	9	1.4		0.0		0.0
miR-191	3	0.4	3	0.5		0.0	1	0.5
miR-193a	1	0.1		0.0		0.0		0.0
miR-193b	1	0.1		0.0		0.0		0.0
miR-194		0.0	1	0.2		0.0		0.0
miR-195	1	0.1		0.0		0.0		0.0
miR-196b		0.0	6	0.9		0.0		0.0
miR-197	3	0.4		0.0		0.0		0.0
miR-199a	16	2.2	141	22.1		0.0	4	1.9

miR-199a*	11	1.5	19	3.0		0.0	1	0.5
miR-199b		0.0		0.0		0.0	1	0.5
miR-200a		0.0	1	0.2		0.0		0.0
miR-200b	2	0.3		0.0		0.0		0.0
miR-200c	14	1.9	12	1.9		0.0		0.0
miR-205	1	0.1		0.0		0.0		0.0
miR-210		0.0	2	0.3		0.0		0.0
miR-214	6	0.8	9	1.4		0.0	2	1.0
miR-214*		0.0	4	0.6		0.0		0.0
miR-221		0.0		0.0	1	1.0	1	0.5
miR-320	1	0.1	13	2.0		0.0	1	0.5
miR-323		0.0		0.0		0.0		0.0
miR-324-5p		0.0	7	1.1	1	1.0	1	0.5
miR-324-3p		0.0	2	0.3		0.0		0.0
miR-335	1	0.1		0.0		0.0		0.0
miR-338		0.0	2	0.3		0.0		0.0
miR-342	1	0.1		0.0		0.0	1	0.5
miR-368	4	0.5	1	0.2		0.0	1	0.5
miR-375		0.0	3	0.5		0.0		0.0
miR-376a	4	0.5	3	0.5		0.0		0.0
miR-409-3p		0.0	1	0.2		0.0		0.0
miR-425-5p		0.0	1	0.2		0.0		0.0
miR-425-3p		0.0	1	0.2		0.0		0.0
miR-432		0.0	7	1.1		0.0		0.0
miR-450		0.0		0.0	1	1.0		0.0
miR-485-5p		0.0	1	0.2		0.0		0.0
miR-493-3p		0.0	4	0.6		0.0		0.0
miR-495	1	0.1	1	0.2		0.0		0.0
miR-497		0.0	1	0.2		0.0	1	0.5
miR-532*		0.0		0.0		0.0	1	0.5
miR-652		0.0	5	0.8		0.0		0.0
<b>739</b>		<b>99.7</b>	<b>637</b>	<b>100</b>	<b>99</b>	<b>100</b>	<b>206</b>	<b>100</b>

## Appendix 1:

### Abstract

#### **Gene Expression Profiling of 24 Novel Sarcoma Cell Lines**

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Brigham and Women's Hospital, Boston, MA Annual meeting USCAP 2007

**Background:** Cell lines derived from fresh tumors have been widely used as experimental models but few sarcoma cell lines exist. Since the process of culturing may alter the phenotype of the cell, a careful molecular characterization of cell lines is useful to establish their validity. The aim of our current study is to examine the gene expression profiles of 24 novel sarcoma cell lines.

**Design:** Oligonucleotide arrays (HEEBO, Stanford) were used to characterize the global gene expression profiles of 24 sarcoma cell lines that included 4 rhabdomyosarcomas (RMS), 2 KIT-positive gastrointestinal stromal tumors (GIST), 1 KIT-negative GIST, 3 synovial sarcomas (SS), 3 malignant peripheral nerve sheath tumors (MPNST), 2 leiomyosarcomas (LMS), 2 liposarcomas (LPS), 2 endometrial stromal sarcomas (ESS), 1 Ewing sarcoma (EWS) and 4 undifferentiated sarcomas developed at Brigham and Women's Hospital. Gene array data from 16 fresh tumors (8 GIST and 8 SS) was included for comparison. Hierarchical clustering and significance analysis of microarray data (SAM) were used for data analysis.

**Results:** Unsupervised hierarchical clustering of the gene array data from the 24 sarcoma cell lines showed tumor-type specific co-clustering in 12 of the 20 cell lines of known sarcoma types in 3 of 4 RMS, 3 of 3 SS, 2 of 2 KIT-positive GIST, 2 of 3 MPNST and 2 of 2 ESS. SAM analysis of the cell lines also revealed gene expression profiles in accordance with data for fresh tumor samples. More significantly, in a separate unsupervised hierarchical clustering that combined the gene array data from 16 fresh tumors (SS and GIST) together with the 24 sarcoma lines, the 2 KIT-positive GIST cell lines clustered together with the 8 fresh frozen tissue GIST while all 3 SS clustered together with the 8 fresh frozen tissue SS.

**Conclusions:** The results of our gene expression analysis of the cell lines reveal that the majority of the 24 sarcoma cell lines exhibit distinct tumor-specific gene expression profiles that are in accordance with the current literature. The comparison of the cell lines and fresh frozen tumor tissues in the case of GIST and SS also indicate that defining gene expression properties of synovial sarcoma and GIST are well conserved in these cell lines, thereby making them highly representative experimental models.

Appendix 2:

manuscript

EPIDERMAL GROWTH FACTOR RECEPTOR (EGFR) EXPRESSION AND GENE  
AMPLIFICATION IN A SPECTRUM OF SPINDLE CELL SOFT TISSUE  
NEOPLASMS: A FLUORESCENCE IN SITU HYBRIDIZATION (FISH) AND  
IMMUNOHISTOCHEMICAL STUDY

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**Running Title: EGFR in Spindle Cell Soft Tissue Neoplasms**

## Abstract

Epidermal growth factor receptor (EGFR) is a transmembrane glycoprotein with tyrosine kinase activity that functions in cell proliferation and survival. EGFR expression and gene amplification has been studied extensively in carcinomas and monoclonal antibodies directed against EGFR have been approved for the treatment of certain types of carcinoma. However, EGFR data in soft tissue neoplasms is limited. Using a variety of benign and malignant spindle cell neoplasms, we assessed EGFR status by fluorescence in-situ hybridization (FISH) using a dual color assay which simultaneously identifies EGFR gene copy number and the centromere of chromosome 7 (EGFR/CEP7, ratio >2 consistent with EGFR amplification; Abbott/Vysis, Abbott Park, IL) and correlated the results with EGFR expression as assessed by immunohistochemistry (IHC) using an EGFR monoclonal antibody (Ventana, Tuscon, AZ). A tissue microarray was constructed from duplicate 0.5 mm cores from formalin-fixed and paraffin-embedded tissues which included 14 synovial sarcomas (SS), 9 dermatofibrosarcoma protuberans with fibrosarcomatous change (DFSP), 5 clear cell sarcomas (CCS), 9 desmoplastic melanomas (DM), 62 malignant peripheral nerve sheath tumors (MPNST; 40 which were associated with neurofibromatosis-1 and 22 sporadic cases), 22 plexiform (PNF), 9 diffuse (DN) and 8 localized neurofibromas (LN), 21 schwannomas (SW), and 3 perineuromas (PN). Immunoreactivity was scored as negative (no staining), 1+, 2+ or 3+. Neoplasms in which the majority of samples showed 2-3+ expression by IHC included MPNST (83% of NF1-associated and 77% of sporadic), 73% of PNF, 100% DN, 56% of DFSP, 100% of PN, and 93% of SS. Of all neoplasms examined, FISH identified only 3 cases which were EGFR amplified, all of which were MPNST (2 NF1-associated, 1 sporadic; EGFR/CEP7 ratio range: 2.2-4.2) and 3 additional MPNST cases which were polysomic for chromosome 7 (3 NF1-associated, CEP7 copy number range: 3.0-5.5). All three of the CEP 7 polysomic cases showed 2-3+ immunoreactivity, while the 3 FISH amplified cases demonstrated 3+ IHC reactivity. The disparity between EGFR protein overexpression and the paucity of EGFR gene amplification may be secondary to some post-transcriptional modification, however further investigation is needed. The finding of EGFR overexpression, especially in malignant neoplasms, deserves further study as EGFR antagonists may be of benefit to patients with soft tissue tumors that express and are dependent on EGFR.

## Introduction

Epidermal growth factor receptor (EGFR), located at 7p12, is a member of a protein tyrosine kinase family and functions as a cell cycle regulatory protein (Kondo and Shimizu, 1983). The receptor is activated by the binding of epidermal growth factor (EGF) and transforming growth factor- $\alpha$  (TGF- $\alpha$ ), which leads to receptor autophosphorylation resulting in cell proliferation and cell survival through inhibition of apoptosis and promotion of angiogenesis (Arteaga, 2003; Arteaga *et al.*, 1988; Hernandez-Sotomayor *et al.*, 1993). EGFR overexpression has been identified in several subsets of malignant neoplasms. For example, 40-80% of non-small cell lung carcinomas have been shown to overexpress EGFR (Rusch *et al.*, 1997).

The multiple cellular signaling interactions of EGFR biology allows for potential EGFR inhibitors to counteract cellular proliferation, angiogenesis, invasion and metastasis. Different pharmaceutical approaches have been used to target either the extracellular ligand-binding domain of the EGFR or the intracellular tyrosine kinase region (Ghosh *et al.*, 2001). The monoclonal antibody cetuximab, which inhibits ligand binding to EGFR, is currently approved for the treatment of colorectal carcinoma, and is in Phase III trials for potential treatment of other subsets of neoplasms, namely carcinomas. Erlotinib is another monoclonal EGFR inhibitor that is approved to treat patients with advanced non-small cell lung cancer, as well as first line treatment for pancreatic cancer. Recent studies have shown that responsiveness to erlotinib therapy may be linked to chromosome 7 polysomy and/or EGFR gene amplification.

There have been few studies evaluating EGFR expression and gene amplification status in sarcomas. However, EGFR immunoexpression levels have been correlated with histologic grade and poor prognosis in adult patients with soft tissue sarcomas (Sato *et al.*, 2005). It is currently unknown if down-regulation of EGFR would benefit patients with either malignant, spindle-cell soft tissue neoplasms or those patients with benign tumors which arise in locations that preclude complete resection.

## Material and Methods

Archival formalin-fixed, paraffin-embedded tissues were obtained from the pathology archives of the collaborative investigators and the correlative hematoxylin and eosin stained slides were reviewed by at least three pathologists who specialize in soft tissue pathology. A tissue microarray (TMA) was constructed with duplicate 0.6 mm cores from the archival material and included MPNST from patients with neurofibromatosis (NF1-related MPNST; n=40), MPNST from patients with no history of neurofibromatosis (sporadic MPNST; n=22), monophasic fibrous synovial sarcoma (SS; n=14), clear cell sarcoma (CCS; n=5), desmoplastic melanoma (DM; n=9), typical schwannoma or cellular schwannoma (SW; n=21), localized neurofibroma (LN; n=8), plexiform neurofibroma (PNF; n=22), diffuse neurofibroma (DN; n=9), perineuroma (PN; n=3), and dermatofibrosarcoma protuberans with fibrosarcomatous change (DFSP/FS; n=9).

Individual four micron sections of the array were deparaffinized and stained using the Benchmark Automated Slide Stainer (Ventana Medical Systems, Tucson, AZ) and the protocol established by the manufacturer for CONFIRM<sup>TM</sup> Anti-Epidermal Growth Factor Receptor (EGFR) (monoclonal-clone 111.6; pre-diluted; Ventana Medical Systems, Tucson, AZ). The procedure includes incubation with Protease 2 for 4 minutes and with primary antiserum for 28 minutes. Antibody was detected using the avidin-biotin complex method, with diaminobenzidine used as the chromagen. The developed slides were counterstained with hematoxylin. Immunoreactivity was scored as negative (no staining), 1+ (weak membranous and/or cytoplasmic staining in <10% of tumor cells), 2+ (weak or partial staining in >10% or strong staining in <50% of tumor cells), or 3+ (strong staining in >50% of tumor cells).

Interphase dual-color fluorescence in situ hybridization (FISH) was performed using directly fluorescent-labeled DNA probes for the EGFR gene (7p12) with a pericentromeric control of chromosome 7 (Abbott/Vysis, Des Plaines, IL). Slides were



baked overnight and deparaffinized-dehydrated through xylene and alcohols. DAKO target retrieval was applied at 95<sup>0</sup> C for 40 minutes. Slides were allowed to cool to room temperature and rinsed in Milli Q water. Next, tissue was incubated for 5 minutes at room temperature with 150 uL of 1:5000 Proteinase K solution, rinsed, dehydrated with alcohols, and dried. Ten uL of probe mixture were applied and the slide was then coverslipped, codenatured at 73 C for 5 minutes, and incubated overnight. The following day the slides were subjected to stringent wash to remove any unbound probe using 2 X SSC and 0.4 X SSC/0.3% NP-40, allowed to air dry completely, and counterstained with DAPI (4', 6-diamidino-2-phenylindole). The signals were visualized on an Axioscop photomicroscope (Zeiss, Oberkochen, Germany) equipped with a triple bandpass filter. Images were captured through a photometric digital cooled CCD camera using a SmartCapture system (Vysis).

In scoring the FISH, 40 tumor nuclei were scored per core, with enumeration of both the centromeric probe, CEP7 (7p11.1-q11.1) which fluoresces green and the EGFR probe (7p12) which fluoresces orange. To avoid nuclear truncation which can occur in tissue sections, only cells containing a minimum of two centromeric signals were included. An EGFR/CEP7 ratio was calculated for each core, with a ratio of <2 equivalent to no EGFR amplification and a ratio of  $\geq 2$  equating with EGFR amplification.

## Results

Examples of EGFR immunohistochemical staining intensities are shown in Figure 1 and the staining intensities for each entity are summarized in Table 1. Of the MPNST, 76% had 2-3+ expression by IHC, with similar results seen in both NF1-associated and sporadic MPNST cases. Of the benign nerve sheath tumors, 100% of DN, 100% of PN, and 73% of PNF demonstrated 2-3+ immunoreactivity, while only 38% of LN and 5% of SW had similar reactivity. The non-nerve sheath tumors that most often showed 2-3+ EGFR immunoreactivity included SS and DFSP (93% and 56%, respectively), while CCS and DM had no EGFR staining in greater than 50% of cases.

EGFR amplification by FISH was identified in only 3 of the neoplasms examined (Figure 2), all of which were malignant peripheral nerve sheath tumors (4.6% of MPNST EGFR amplified; 2 NF1-associated, 1 sporadic; EGFR/CEP7 ratio range: 2.2-4.2). Polysomy of chromosome 7 was identified in 3 additional cases, all of which were NF1-associated malignant peripheral nerve sheath tumors (chromosome 7 copy number range: 3.0-5.5). The FISH-amplified cases demonstrated 3+ IHC reactivity and the CEP 7 polysomic cases showed 2-3+ immunoreactivity. All other neoplasms had no evidence of EGFR amplification (EGFR/CEP7 ratio range: 1.0-1.8).

## Discussion

A subset of both benign and malignant spindle cell lesions included in this study showed significant protein overexpression (2-3+ immunoreactivity) of EGFR. EGFR gene amplification by FISH was only identified in rare examples of MPNST, all of which showed 3+ staining for EGFR. These findings suggest that gene amplification is not the mechanism of increased EGFR protein expression, and that transcriptional or post-transcriptional processes are likely involved. Other studies focusing on EGFR gene

amplification status in solid malignancies including lung, prostate, bladder, head and neck, and gastrointestinal tumors have all reported low incidences of gene amplification relative to receptor overexpression, implying that gene amplification is not the prevailing mechanism of EGFR overexpression (Spaulding and Spaulding, 2002). EGFR signaling may additionally be increased by a number of mechanisms in addition to high expression levels of EGFR, including receptor mutations, heterodimerization with other members of this receptor family such as HER2 (erbB2), increased expression of (autocrine/ paracrine) ligands, and alterations in molecules that control receptor signaling output (Arteaga, 2002).

An optimized immunohistochemistry assay for EGFR has been developed in colorectal, head and neck, and other tumors that are known to express EGFR, and this assay is currently being used in colorectal cancer trials of select patients for treatment (Spaulding and Spaulding, 2002). However, to date, no clear association has been established between EGFR expression levels and response to EGFR-targeted agents.

The results reported here of EGFR expression and genomic amplification status in soft tissue tumors parallel the findings in the majority of studies evaluating EGFR expression/amplification in carcinomas. Subsets of patients with malignant soft tissue neoplasms or those with benign tumors which arise in locations which preclude complete resection may be suitable candidates for trials with anti-EGFR chemotherapeutics.

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